

Linking Archaeal Molecular Diversity and Lipid Biomarker Composition in a Hypersaline Microbial Mat Community

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Lipid biomarkers for discrete microbial groups are a valuable tool for establishing links to ancient microbial ecosystems. Lipid biomarkers can establish organism source and function in contemporary microbial ecosystems (membrane lipids) and by analogy, potential relevance to the fossilized carbon skeletons (geolipids) extracted from ancient sedimentary rock. The Mars Exploration Rovers have provided clear evidence for an early wet Mars and the presence of hypersaline evaporitic basins. Ongoing work on an early Earth analog, the hypersaline benthic mats in Guerrero Negro, Baja California Sur, may provide clues to what may have evolved and flourished on an early wet Mars, if only for a short period.

Cyanobacterial mats are a pertinent early Earth analog for consideration of evolutionary and microbial processes within the aerobic photosynthetic and adjacent anoxic layers. Fluctuations in physio-chemical parameters associated with spatial and temporal scales are expressed through vast microbial metabolic diversity. Our recent work hopes to establish the dynamic of archaeal diversity, particularly as it relates to methane production in this high sulfate environment, through the use of lipid biomarker and phylogenetic analyses. Archaeal 16S rRNA and *mcrA* gene assemblages, demonstrated distinct spatial separation over the 130 mm core of at least three distinct genera within the order Methanosarcinales, as well as an abundance of uncultured members of the Thermoplasmatales and Crenarchaeota. Ether-bound lipid analysis identified abundant *O*-alkyl and *O*-isopranyl chains throughout the core, and the presence of *sn*-2 hydroxyarchaeol, a biomarker for methylotrophic methanogens. A unique ether isoprenoid chain, a C_{30:1}, possibly related to the geolipid squalane, a paleobiomarker associated with hypersaline environments, was most abundant within the oxic-anoxic transition zone.

